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ORIGINS OF SOCKEYE AND CHUM SALMON SEIZED
FROM THE CHINESE VESSEL *YING FA*

by

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ABSTRACT

Samples of chum (*Oncorhynchus keta*) and sockeye (*O. nerka*) salmon seized from the stateless fishing vessel *Ying Fa* were analyzed to determine their region of origin using genetic stock identification (GSI), otolith marks, parasite analysis, and scale data. Based on GSI, the chum salmon samples originated in Russia, 86%; Japan, 2%; western Alaska, 2%; Alaska Peninsula and Kodiak, 8%; and British Columbia, 2%. Origins of the sockeye salmon sample were not so clear because there was some disagreement between the parasite data and the GSI and scale data. Results of parasite analysis suggested the sample was nearly all of Alaskan origin, with at least 15% coming from Bristol Bay. The GSI analysis indicated that 30% of the sockeye salmon originated in Russia and 70% in North America. The scale analysis showed that 97% of the sockeye salmon sample were ocean age 3, whereas the return to Bristol Bay in 1999 was approximately 70% ocean age 2 fish.

INTRODUCTION

On 24 April 1999, the fishing vessel *Ying Fa* was intercepted by the U.S. Coast Guard (USCG) after being sighted in international waters by a Canada Department of Fisheries and Oceans (CDFO) patrol aircraft approximately 400 miles southwest of Attu Island at 48E 41N and 163E 23N (Fig. 1). The vessel was fishing illegally (Magnuson-Stevens Fishery Conservation and Management Act 1996), with over 10 nautical miles of driftnet and over 6 tons of frozen salmon (*Oncorhynchus* spp.) onboard. Although the F/V *Ying Fa* had been previously registered in the People's Republic of China (PRC), the PRC government on 30 April 1999 refuted the vessel's registration, and the United States assimilated the *Ying Fa* as stateless. Chuck Guthrie from the Auke Bay Laboratory (ABL) identified the catch as being approximately half sockeye salmon (*O. nerka*) and half chum salmon (*O. keta*): 97 chum salmon and 106 sockeye salmon were in the round. The remainder of the fish onboard were gutted and boxed. All whole fish were retained for genetic sampling. Mr. Guthrie collected a total of 299 chum salmon and 290 sockeye salmon from the vessel hold on 3 May, which were shipped to ABL for stock identification using scale characteristics, otolith marks, parasites, and genetics.

Otolith marks and scale growth rings can also aid in determining the origins of salmon. Hatcheries purposely regulate temperature to mark otoliths of young salmon. Some chum salmon hatcheries in southeastern Alaska and British Columbia release large numbers of thermally marked fry that can be definitively identified from otoliths sampled later. Scale growth rings show the amount of time spent in fresh water and saltwater, indicating area of origin because certain regions produce fish of specific freshwater and marine ages.

Parasites acquired during freshwater residence of sockeye salmon can serve as useful markers in mixed-stock fisheries. Unlike most other management tools for stock separation, parasite markers require no initial tagging because the tag is acquired naturally during early life. Parasite fauna reflect differences in the stream of origin such as habitat, diet, limnology, or presence of

intermediate hosts. A few parasites persist for a year or more, are not lost during the transition to saltwater, and have a disjunct distribution. Studies by Canadian, Russian, U.S., and Japanese fishery agencies over the last 40 years have determined that six parasite genera meet the criteria for use as marker parasites in sockeye salmon: *Myxobolus*, *Triaenophorus*, *Philonema*, *Truttaedacnitis*, *Henneguya*, and *Echinorynchus*. Using the presence or absence of each parasite, certain stocks in the baseline could be eliminated as contributors to a mixed-stock fishery.

Genetic stock identification relies on genetic differences among stocks in relative frequencies of protein-coding genes detected by allozyme electrophoresis. A genetic baseline has been constructed from potentially contributing stocks around the North Pacific Ocean. A comprehensive genetic baseline for chum salmon has been developed from data provided by various state and federal agencies from Japan, Russia, Canada, and the United States (Kondzela et al. 1994; Phelps et al. 1994; Wilmot et al. 1994; Winans et al. 1994; Seeb et al. 1995; Urawa et al. 1998). A comprehensive genetic baseline for sockeye salmon had not been developed prior to this study.

METHODS

Age and Size Composition

First, all fish were weighed and measured for length, tip of snout to fork of tail. Sex and maturity were determined when gonads were present. Two scales were collected from each fish for age determination. The first 50 sockeye and chum salmon stomachs sampled were retained for diet studies, and otoliths were collected from the chum salmon to check for hatchery thermal marking. We list only the ocean age, i.e. the number of marine annuli on the scales. In the western North Pacific Ocean, chum salmon may not complete the annulus until June (Sakurai 1996). Sockeye salmon usually complete the annulus earlier than chum salmon (Birman 1960; Bilton and Ludwig 1966). In order to avoid underestimating the ocean age of fish that had not begun or completed the formation of the last annulus, we added one to the number of marine annuli already formed on the scale.

Parasite Stock Identification

Sockeye salmon heads (including a large amount of adjacent flesh) and internal organs were removed for parasite analysis. After an examination of the flesh for parasites, the brain was removed and examined for the myxosporidian *Myxobolus* as described in Moles et al. (1990). The internal organs were soaked for several minutes in warm water and examined for mesenteric parasites. Stomach contents were preserved in formalin. The viscera were digested in pepsin and the resulting solution examined under a dissecting microscope for acanthocephalans and nematodes. A total of 60 sockeye salmon were examined for parasites. This sample size detects with an accuracy of 95% the presence of parasites prevalent in 5% or

more of the population (Canadian Department of Fisheries and Oceans 1984). We did not examine for the marker parasite *Henneguya*.

Chum salmon, which migrate to sea soon after emergence, pick up few parasites during freshwater residence. The use of marker parasites to evaluate freshwater origin was not pursued.

Genetic Stock Identification

Samples of tissue from the heart, liver, muscle, and eye were taken from whole fish, and muscle and eye from gutted fish, placed in individual tubes, and frozen at -80°C until electrophoretic analysis. Protein electrophoresis was used to identify genotypes for the 20 loci available in the Pacific Rim chum salmon baseline (Seeb et al. 1995; Wilmot et al. 1998; Seeb and Crane 1999). Electrophoretic analysis followed procedures described by Aebersold et al. (1987) and Harris and Hopkinson (1976), and results are reported using the genetic nomenclature of the American Fisheries Society (Shaklee et al. 1990). Specific tissues and buffers used to interpret genetic variation at each locus for chum salmon follow Kondzela et al. (1994), except that due to lack of heart and liver tissue in many samples, eye tissue was used for loci *MPI** and *sIDHP-2** with TG and CAME7.4 buffers, respectively, and muscle tissue was used for *PEPA** with R and MF buffers. Specific tissues and buffers used to interpret genetic variation at 72 sockeye salmon loci follow Guthrie et al. (1994).

The chum salmon baseline included the 77 populations used by the National Marine Fisheries Service (NMFS) to estimate the regional origin of chum salmon incidentally caught in the Bering Sea trawl fishery (Wilmot et al. 1998). This baseline includes representative populations from Japan, Russia, western Alaska, fall Yukon River, Alaska Peninsula, Prince William Sound–southeastern Alaska, British Columbia, and Washington. Simulations have shown that the baseline provides enables discrimination of these eight regions with 82–97% accuracy (Wilmot et al. 1998; Seeb and Crane 1999). A coastwide baseline was constructed for sockeye salmon using data from Russia (ABL, unpublished data), Bristol Bay (Varnavskaya et al. 1994; Everett and Wilmot, unpublished data), western and southcentral Alaska (Alaska Department of Fish and Game [ADF&G], unpublished data), southeastern Alaska-British Columbia (Guthrie et al. 1994; Wood et al. 1994; ABL, unpublished data; Wood-CDFO unpublished data), and Washington (Winans et al. 1996). Table 1 lists the site names and source of data. The genotypic frequency of the locus *PGM-1** could not be determined due to null allele variation and was therefore treated as a phenotypic character. Geographical structure was examined by constructing a neighbor-joining tree (Saitou and Nei 1987) for 165 populations of Pacific Rim sockeye salmon using the 14 common loci and Cavalli-Sforza and Edwards (1967) chord distance (Fig. 2).

Conditional maximum likelihood estimates (MLE) of stock composition of the confiscated samples were calculated using the CONSQRT program of Masuda et al. (1991). Standard errors of stock composition estimates were determined by 500 bootstrap resamplings of baseline and mixture samples (Efron and Tibshirani 1986). Simulation studies were conducted with the sockeye salmon baseline to evaluate the reliability of stock composition estimates using

SIMSQURT (Masuda et al. 1991). Simulated baseline samples of sizes equal to actual baseline samples were generated by resampling. Mixture samples, comparable in size to that available and composed of 100% of stocks from a given region (equal proportions by the region's baseline stocks) were simulated from baseline allele frequencies. Genotypes of individuals in these hypothetical mixtures of known composition were generated from baseline allele frequencies assuming independence of loci and Hardy-Weinberg equilibrium. The SIMSQURT program calculated the MLE of stock composition for each simulated set of baseline and mixture samples, and the average MLE's of regional composition were compared with the true contribution. The 100% simulations were repeated for each region.

CHUM SALMON

RESULTS

Age and Size Composition

Age composition of the chum salmon samples was 25% ocean age 3 ($N = 68$), 69% ocean age 4 ($N = 186$), and 6% ocean age 5 ($N = 17$) fish. No thermally marked otoliths were found in the chum salmon samples (Peter Hagen, ADF&G). Average length and weight for the chum salmon samples were 510 ± 7 mm and 1.33 ± 0.03 kg for ocean age 3 fish, 534 ± 4 mm and 1.58 ± 0.04 kg for ocean age 4 fish, and 560 ± 16 mm and 1.77 ± 0.18 kg for ocean age 5 fish (Table 2). The chum salmon samples were classified as maturing due to the presence of identifiable testes in the males and eggs nearing 1 mm in size in the females.

Genetic Stock Identification

Regional stock group estimates (Table 3) indicated most of the chum salmon ($86\% \pm 6\%$) were from Russian populations, with nearly half from rivers in the northern Sea of Okhotsk. More than one-quarter were from populations on the western Kamchatka Peninsula. Only $2\% \pm 2\%$ were from Japanese populations. A small fraction ($8\% \pm 4\%$) were from Alaska Peninsula and Kodiak Island populations. No significant contributions were made by populations from Japan, western Alaska, fall Yukon River stocks, or from Prince William Sound and southward in North America.

DISCUSSION

Age Composition

Age composition of the chum salmon aboard the F/V *Ying Fa* was 25% ocean age 3, 69% ocean age 4, and 6% ocean age 5. Age composition like this which is skewed toward older fish generally indicates fish destined to spawn in northern areas of Asia or North America

(Sano 1966; Helle 1984). However, after about 1980, chum salmon from both southern and northern areas in Asia and North America have matured at older ages (Kaeriyama 1989, 1996; Ishida et al. 1993; Helle and Hoffman 1995, 1998). Therefore, without more definitive baseline information on age at maturity from spawning populations in 1999, area of origin based on age cannot be predicted with certainty.

Genetic Stock Identification

The accuracy of the chum salmon genetic baseline has been tested widely and used in mixed-stock analyses including the chum salmon bycatch in the sockeye salmon fisheries near south Unimak and Shumagin Islands along the southern Alaska Peninsula (Seeb and Crane 1999), the chum salmon bycatch in the Bering Sea trawl fishery for walleye pollock (Wilmot et al. 1998), and a high seas sample of juvenile chum salmon (Urawa et al. 1998; Winans et al. 1998). The estimated presence of nearly 88% Asian-origin chum salmon in the catch was expected given the location where the F/V *Ying Fa* was fishing. Also, the small proportion of Alaska and British Columbia origin fish is consistent with results from the analyses of the Bering Sea trawl fishery (Wilmot et al. 1998) and the high seas samples by Urawa et al. (1998) and Winans et al. (1998). The presence of chum salmon from central and southeastern Alaska and British Columbia hatcheries in the waters on both the Pacific and Bering Sea sides of the Aleutian Islands was confirmed by the recovery of fish with thermally marked otoliths (Farley and Munk 1997).

SOCKEYE SALMON

RESULTS

Age and Size Composition

Freshwater ages of sockeye salmon samples varied with small numbers of 0-age fish among 1-year, 2-year, and 3-year fish. The marine age was distinctive, however: 96% were ocean age 3 ($N = 261$) and only small numbers of ocean age 4 (3.6%, $N = 10$) and ocean age 2 (0.04%, $N = 1$). The sockeye salmon samples averaged 548 ± 3 mm with an average weight of 1.98 ± 0.02 kg (Table 2). Like the chum salmon, sockeye salmon samples were classified as maturing.

Parasite Stock Identification

Nine (15%±5%) of the 60 sockeye salmon examined contained the cestode *Trianeophorus*, and the nematode *Philonema* was found in the mesenteries of all but one fish (98%). Three other marker parasites were not detected in any sample: the brain parasite *Myxobolus*, the intestinal nematode *Truttaedacnitis*, and the acanthocephalan worm *Echinorhynchus*.

Genetic Stock Identification

We gathered genetic data for 165 populations: 7 populations from Russia, 30 from western Alaska, 52 from southcentral Alaska, 37 from southeastern Alaska, 34 from British Columbia, and 5 from Washington (Table 1). Data for only 14 loci were available across all regions: *sAAT-1,2**; *mAAT-1**; *ALAT**; *GPIB-1,2**; *sIDHP-1**; *sIDHP-2*; *LDHB-1**; *LDHB-2**; *MPI**; *sMDHA-1,2*; *sMDHB-1,2*; *PGM-1**; *PGM-2**; and *sSOD-1**. Data for 10 other variable loci were missing: Russia (*sAH-1**, *PEPC**, *PEPLT**, *TPI-1,2**, *TPI-3**, and *TPI-4**); Bristol Bay (*PEPC**); British Columbia (*GPIA**, *PEPD-1**, *TPI-1,2**, *TPI-3**, and *TPI-4**); and Washington State (*sMEP-1**, *mMEP-1**, and *PEPD-1**).

The neighbor-joining tree (Fig. 2) shows that populations from Russia displayed some clustering, but that the populations from southwestern, southcentral, and southeastern Alaska and British Columbia were scattered widely within the tree. Five of the Russian populations are contained within the uppermost cluster along with Iliamna and Nushagak Rivers from Bristol Bay and Jim Creek in southcentral Alaska. Hairusova River (western Kamchatka) is contained within the next large cluster, with numerous southcentral Alaska and a few western Alaska populations.

The 100% simulation studies (Table 4) showed that if the F/V *Ying Fa* catch had been composed of equal proportions of the baseline stocks of Russia alone, 85.4%±6.8% would have been estimated correctly as originating in Russia. Corresponding values for the other regions were lower: western Alaska at 61.1%±12.8%, southcentral Alaska at 78.9%±8.3%, southeastern Alaska at 67.7%±9.8%, British Columbia at 75.2%±8.8%, and Washington at 74.4%±11.1%. More than 14% of the Russian fish were misallocated to North American stocks: 7.8% to southcentral Alaska, 3.5% to British Columbia, 2.3% to western Alaska, and 1% to southeastern Alaska. None of the North American regions misallocated substantial amounts to Russia; western Alaska was the highest at 3.4%.

When the results of the 100% simulations were summed by continent, accuracy improved substantially for North American stocks (Table 5). Correct allocation to continent for Russian stocks remained at 85.4%±6.8%, but that for western Alaska changed to 96.6%±4.2%, for southcentral Alaska to 98.7%±2.4%, for southeastern Alaska to 99.4%±1.1%, for British Columbia to 98.9%±1.8%, and for Washington at 100.0%±0.0%.

The estimates of the origins of the sockeye salmon by region were Russia, 30.2%±15.5%; western Alaska, 14.9%±6.7%; southcentral Alaska, 36.0%±14.1%; southeastern Alaska, 2.4%±2.3%; British Columbia, 15.4%±5.3%; and Washington, 1.1%±1.6% (Table 6). When the estimates were summed by continent rather than by region, the results were Russia 30.2%±15.5% and North America 69.8%±15.5%.

DISCUSSION

Age Composition

Freshwater ages were highly variable and included ages 0, 1, 2, and 3. Individuals from both Russian and North American populations have these freshwater ages. However, the marine ages of sockeye salmon on the F/V *Ying Fa* were distinctive: more than 96% were ocean age 3 fish and less than 4% were ocean age 2 or 4. Ocean age 3 salmon as age 2, ordinarily occur in all regions (Burgner 1991).

Preliminary results of the weighted Bristol Bay-wide estimate of the age structure of sockeye salmon returning to Bristol Bay in 1999 (CPUE-weighted Port Moller samples, $N = 4400$) indicate more than 70% were ocean age 2. As a result of size selectivity of the Bristol Bay gill-nets, this percentage may have been underestimated by 5–10% (pers. com. Michael Link ADF&G). Therefore, the ocean age composition (mainly ocean age 3) of sockeye salmon on the F/V *Ying Fa* was very different from that of the 1999 Bristol Bay return.

Ocean age 4 sockeye salmon are not common in western Alaska, central Alaska, British Columbia, Washington, or Japan, but occur regularly in the Bolshaya River of the Kamchatka River system in Russia. The age groups may distribute differently in the ocean, and if so, little can be inferred from the age composition.

Parasite Stock Identification

Nine of the 60 fish (15%) examined had the cestode *Trianeophorus*. The obligatory definitive host of this parasite is the northern pike, *Esox lucius*. Sockeye salmon become infected with the tapeworm only in lakes where sockeye salmon and pike are sympatric—something that had been reported only from the river systems in Bristol Bay (Margolis 1963, 1998). However, the most recent sampling in most of the populations was 40 years ago, and distribution changes are possible. Records of ADF&G Sport Fish Division indicate the presence of northern pike in other western and southcentral drainages (Howe et al. 1998).

The presence of the nematode *Philonema* in the mesenteries of all but one fish in the sample argues against the Fraser River or Pacific Northwest origin of these fish. Fish in these systems are largely devoid of *Philonema*, probably due to the unique life cycle of Fraser River sockeye salmon (Bailey and Margolis 1987).

The absence of the remaining marker parasites also helps to eliminate some stocks. A fair proportion of sockeye salmon of sampled Asian stocks (Kamchatka River and Kuril Lake) are typically infected with the brain parasite *Myxobolus*, as are sockeye salmon from stocks east

of 147EW (Moles et al. 1990; Moles and Jensen, in prep.). Intestines of sockeye salmon (1%-2%) from Asian stocks are also infected with the nematode *Truttaedacnitis*, which is not present in North American stocks (Margolis 1963), and the acanthocephalan worm *Echinorhynchus* (Margolis 1965).

We did not examine for the sixth marker parasite, *Henneguya*, which is present in southeastern Alaska, Canadian, and Pacific Northwest stocks and largely absent from other sockeye salmon streams. However, the sampling crew would certainly have noticed the presence of the large muscle cysts formed by the parasite.

Genetic Stock Identification

In contrast to the chum salmon genetic baseline, this study is the first attempt at assembling a Pacific Ocean-wide genetic baseline for sockeye salmon. The chum salmon baseline includes 20 genetic characters, but only 14 characters were available for the sockeye salmon genetic baseline. The presence of geographical structuring using the 14 loci common to all stocks was not evident as shown by the neighbor-joining tree (Fig. 2), except for the clustering of Russian stocks near the top. The 100% simulation tests did show success can be expected in estimating Asia versus North American origin (Table 5). However, attempts to estimate origin by region within North America were not so reliable (Table 4). Significant proportions of all regions within North America were misallocated to other regions within North America. Approximately 15% of the Russian fish were misallocated to North America and very small proportions of any of the North American regions were misallocated to Russia. As a result, 30% of the sample from the F/V *Ying Fa* allocated to Russia appears sound, as does the approximately 70% allocated to North America.

In our efforts to synthesize the three lines of data (age and size, parasites, and genetics), it became clear that determining the origins of the sockeye salmon sample from the F/V *Ying Fa* would not be so distinct as that for the chum salmon sample. The parasite data indicated at least 15% of the sample came from Bristol Bay due to the presence of the cestode *Trianeophorus*. However, the prevalence of *Trianeophorus* in Bristol Bay sockeye salmon is highly variable, making more specific quantitative estimates of stock composition unreliable (Margolis 1998). The other parasite markers suggest few or no fish in the sample from much of Russia, southeastern Alaska, Fraser River, or Washington. The absence of the brain parasite *Myxobolus* suggests North American origin because the largest stocks in Russia (Kamchatka River and Kuril Lake) are infected. However, not all stocks in Russia are known to be infected. The predominance of ocean age 3 fish (96%) in the sample argues against Bristol Bay origin for most of the sample. The 1999 Bristol Bay sockeye salmon return was predominately ocean age 2 fish (>70%). The genetic data indicated that 30% of our samples were of Russian origin and 70% of North American origin. Because the program tends to underestimate the Russian proportion, we felt that these were reasonable estimates. The

genetic data do agree with the parasite data in that approximately 15% of the sample came from Bristol Bay. However, due to the level of misallocation between the North American regions, it is difficult to determine what level of confidence should be placed in this figure.

The use of genetic, parasite, and scale data show the potential for discriminating among stocks of sockeye salmon. However, the database is incomplete for genetic data, and needs updating for the parasite and scale data. Obtaining data from all regions for the additional 10 variable loci should substantially increase our ability to discriminate between regions within North America. Efforts underway by a number of federal and state agencies in the United States and Canada to develop a microsatellite DNA baseline also holds promise for more reliable stock identification. A concerted effort should be made by the Parties of NPAFC to rectify this situation soon.

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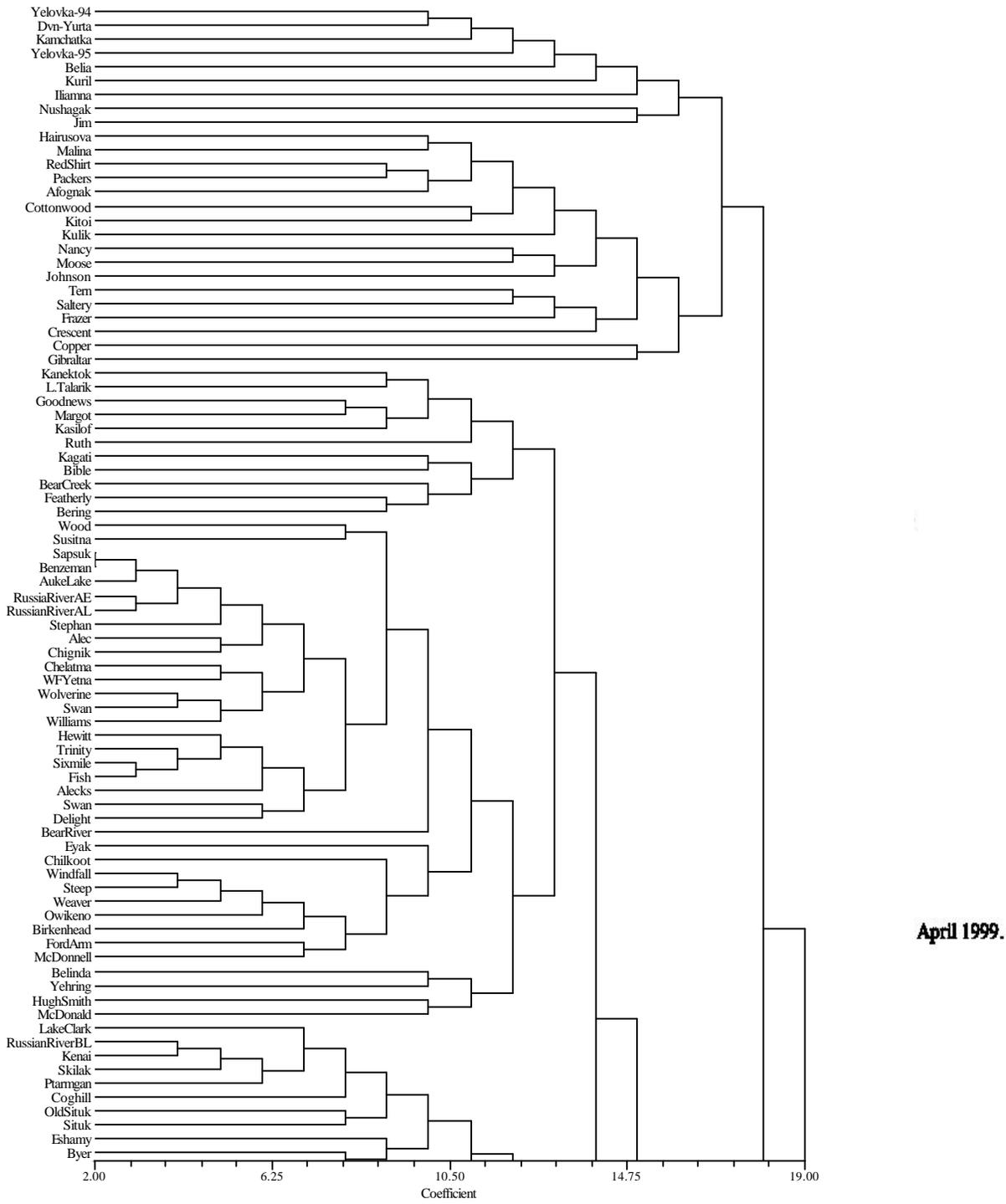


Figure 2. Neighbor-joining tree of 165 sockeye salmon populations using 14 loci and Cavalli-Sforza and Edwards chord distance (1967).

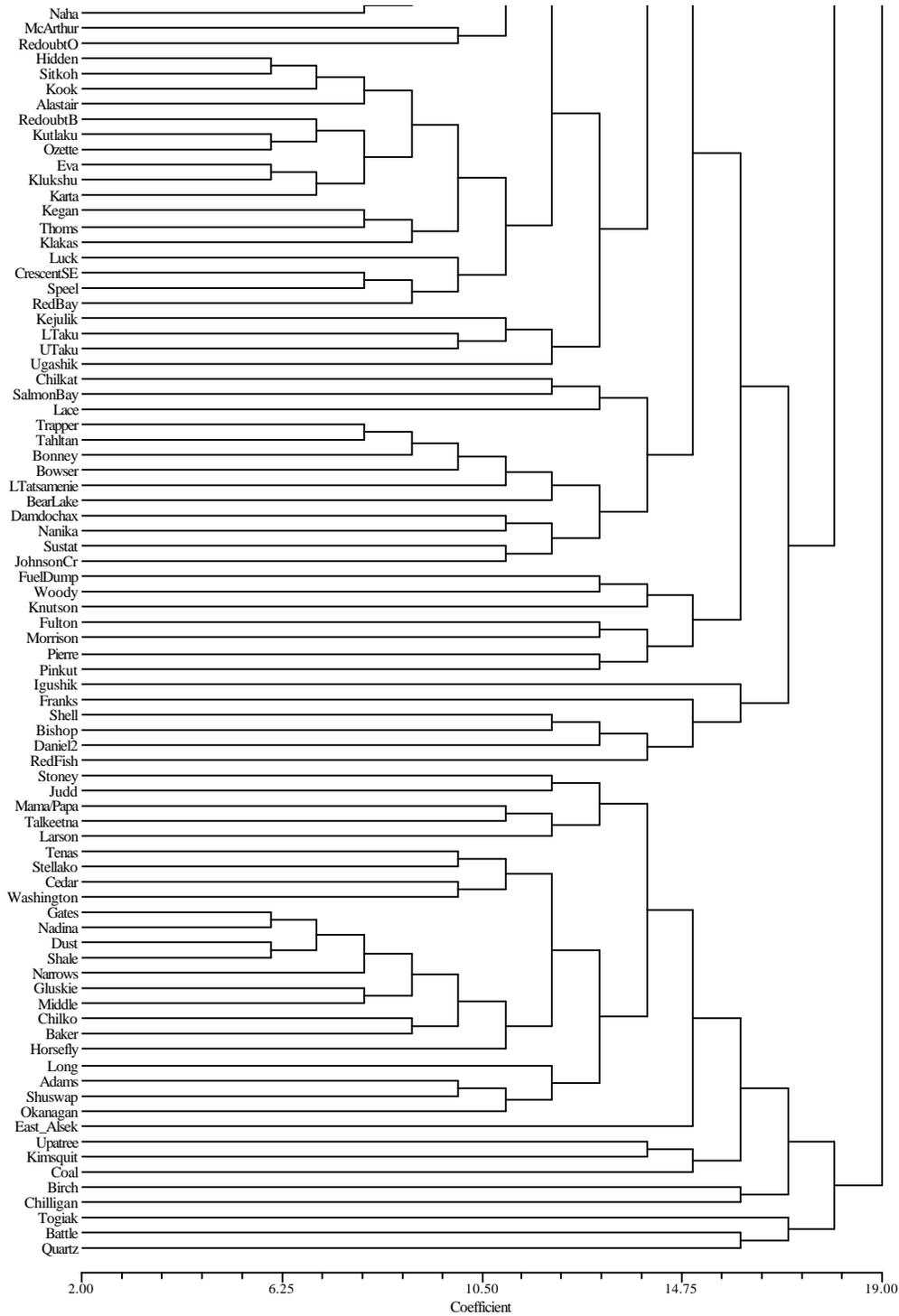


Figure 2. Continued.

Table 1. Sockeye salmon populations sampled for genetic analysis and the source of the data.

Site	Source	Site	Source
<u>Russia</u>			
		Coghill Lake	4
Yelovka River-94	1	Mama/Papa Bear Lake	4
Yelovka River-95	1	Talkeetna River Slough	4
Kamchatka River	1	Stephan Lake	4
Dvn-Yurta	1	Susitna River Slough	4
Belaia River	1	Red Shirt Lake	4
Kuril Lake	1	Birch Creek	4
Hairusova River	1	Byers Lake	4
<u>Western Alaska</u>			
		Larson Lake	4
Stoney River	2	Chelatna Lake	4
Kanektok River	2	WF Yetna River	4
Kagati River	2	Hewitt/Whiskey Lake	4
Goodnews River	2,4	Shell Lake	4
Togiak River	2	Trinity/Movie Lake	4
Igushik River	2	Judd Lake	4
Wood River	2	Sixmile Creek	4
Nushagak River	2	Jim Creek	4
Battle Creek	2	Fish Creek	4
Kulik Creek	2	Cottonwood Creek	4
Belinda Creek	2	Nancy Lake	4
Copper River	2,3	Swanson River	4
Gibraltar Creek	2,3	Bishop Creek	4
Iliamna River	2,3	Daniels Lake	4
Lower Talarik Creek	2	Russian River Above/Early	4
Fuel Dump Island	3	Russian River Above/Late	4
Knutson Creek	3	Russian River below	4
Woody Island	3	Kenai River	4
Lake Clark	2	Skilak Lake Outlet	4
Margot Creek	2	Quartz Creek	4
Upatree Creek	2	Ptarmigan Creek	4
Bear Creek	2	Hidden Creek	4
Bible Creek	2	Tern Lake	4
Featherly Creek	2	Moose Creek	4
Franks Creek	2	Johnson/Railroad Creek	4
Kejulik River	2	Kasilof River	4
Ruth River	2	Coal Creek	4
Ugashik River	2	Chilligan River	4
Bear River	2	Packers Lake	4
Sapsuk Lake	2	Crescent Lake	4
<u>Southcentral Alaska</u>			
		McArthur River	4
Eyak Lake	4	Wolverine Creek	4
Bering Lake	4	Delight Lake	4
Eshamy Lake	4	Frazer River	4

Table 1. Continued.

Site	Source	Site	Source
Little Kitoi	4	Steep Creek	1,5
Afognak Lake	4	British Columbia	
Saltery Creek	4	Klukshu Lake	6
Malina Lake	4	Bowser Lake	6,7
Alec River	4	Bonney Lake	6,7
Chignik Lake	4	Damdochax Lake	6,7
Southeastern Alaska		Alastair Lake	6,7
Luck Lake	5	Williams Creek	6,7
Kegan Lake	5	McDonnell Lake	6,7
Chilkat Lake	5	Swan Lake	6,7
Klakas Lake	5	Bear Lake	6,7
Chilkoot Lake	5	Sustat River	6
Yehring Creek	5	Johnson Creek	6
Sitkoh Lake	5	Nanika River	6,7
Windfall Lake	5	Fulton River Channel	6
Old Situk River	1	Pierre Creek	6,7,8
Redoubt Lake Beach	1	Pinkut River Channel	6
Ford Arm Lake	1	Morrison River	6,7
Redoubt Lake Outlet	1	Kimsquit Lake	6,7
Redfish Lake	1	Tenas Lake	6,7
Benzeman Lake	1	Owikeno Lake	6,7
Eva Lake	1	Long Lake	6,7
Kook Lake	1	Weaver Channel	6
Lace River	1	Birkenhead River	6
East Alsek River	1,5	Gates Channel	6
Lower Taku River	5	Chilko Lake	6
Upper Taku River	5	Horsefly River	6,7
Little Trapper	1,5	Stellako River	6
Little Tatsamenie	1,5,6	Nadina Channel	6
Tahltan Lake	1,6	Gluskie Creek	6
Crescent Lake-SEAK	1	Dust Creek	6
Alecks Lake	1,5	Shale Creek	6
Naha River	1,5	Narrows Creek	6
Hugh Smith Lake	1,5	Middle River	6
Karta River	1,5	Adams River	6,7
Kutlaku Lake	1,5	Shuswap River	6,8
McDonald Lake	1,5	Washington	
Red Bay Lake	1,5	Baker Lake	8
Salmon Bay Lake	1,5	Cedar River	8
Speel Lake	1,5	Okanagan River	6,7,8
Thoms Lake	1,5	Ozette Lake	8
Situk Lake	1,5	Lake Washington	8
Auke Lake	1,5		

1 C.M. Guthrie, ABL, Juneau, AK, unpublished data 5 Guthrie et al. (1994)

2 W.J. Spearman, USFWS, Anchorage, AK unpublished data 6 Wood et al. (1994)

3 Varnavskaya et al. (1994)

7 C. Wood, CDFO, Nanino, BC unpublished data

4 W. Templin, ADF&G, Anchorage, AK unpublished data 8 Winans et al. 96)

Table 2. Size composition of sockeye and chum salmon sampled onboard the F/V *Ying Fa*. Mean and 95% confidence interval of the mean for length and weight data by ocean age. TSFT = tip of snout to fork of tail.

Species	Ocean Age	Sample Size	TSFT length (mm)	Weight (kg)
Sockeye	3	246	548±3	1.98±0.02
Chum	3	65	510±7	1.33±0.03
	4	185	534±4	1.58±0.04
	5	15	560±16	1.77±0.18

Table 3. Estimated regional proportions, standard deviations, numbers, and 90% confidence intervals of chum salmon collected from the confiscated catch of the F/V *Ying Fa*.

Region	Estimated Proportion	S.D.	N	90% C.I.
Japan	0.020	0.023	6	0 – 17
Russia	0.858	0.055	257	230 – 284
Western Alaska	0.020	0.026	6	0 – 19
Fall Yukon	0.000	0.001	0	0
Alaska Peninsula/ Kodiak	0.081	0.041	24	4 – 45
Prince William Sound SE Alaska	0.001	0.018	0	0 – 9
British Columbia	0.020	0.018	6	0 – 15
Washington	0.000	0.000	0	0
Total			299	

Table 4. Mean estimated proportion of sockeye salmon by region for 500 bootstrap simulations where each region comprises 100% of the mixture (N=300). Cells with asteriks are the correct allocation and should equal 1. Standard deviations are in parentheses.

Estimated Region	100% Simulations		
	Russia	Western Alaska	Southcentral Alaska
Russia	0.8538* (0.0679)	0.0228 (0.0312)	0.0780 (0.0544)
Western Alaska	0.0341 (0.0424)	0.6107* (0.1280)	0.1832 (0.0900)
Southcentral Alaska	0.0127 (0.0236)	0.0891 (0.0681)	0.7892* (0.0832)
Southeast Alaska	0.0057 (0.0110)	0.0701 (0.0630)	0.1162 (0.0603)
British Columbia	0.0107 (0.0178)	0.0461 (0.0501)	0.0803 (0.0530)
Washington State	0.0000 (0.0000)	0.0022 (0.0066)	0.0206 (0.0228)

Estimated Region	Southeastern Alaska	British Columbia	Washington
Russia	0.0100 (0.0169)	0.0349 (0.0304)	0.0005 (0.0017)
Western Alaska	0.0752 (0.0636)	0.0905 (0.0578)	0.0063 (0.0137)
Southcentral Alaska	0.0509 (0.0440)	0.0520 (0.0342)	0.0061 (0.0120)
Southeast Alaska	0.6765* (0.0975)	0.1140 (0.0629)	0.0174 (0.0261)
British Columbia	0.0860 (0.0591)	0.7516* (0.0882)	0.0254 (0.0303)
Washington State	0.0660 (0.0459)	0.1669 (0.1070)	0.7442* (0.1111)

Table 5. Mean estimated proportion of sockeye salmon by continent for 500 bootstrap simulations where each region comprises 100% of the mixture (N=300). Cells with asteriks are the correct allocation and should equal 1.0000. Standard deviations are in parentheses.

100% Simulations	Estimates by Continent	
	Asia	North America
Russia	0.854 (0.068)*	0.146 (0.068)
Western Alaska	0.034 (0.042)	0.966 (0.042)*
Southcentral Alaska	0.013 (0.024)	0.987 (0.024)*
Southeastern Alaska	0.006 (0.011)	0.994 (0.011)*
British Columbia	0.011 (0.018)	0.989 (0.018)*
Washington	0.000 (0.000)	1.000 (0.001)*

Table 6. Estimated regional and continental origins of sockeye salmon seized from the Chinese vessel F/V *Ying Fa*. Standard deviations in parentheses were calculated from 500 bootstrap resamplings of the baseline and mixture samples.

Region	Estimate
Russia	0.302 (0.155)
Western Alaska	0.149 (0.067)
Southcentral Alaska	0.360 (0.141)
Southeastern Alaska	0.024 (0.023)
British Columbia	0.154 (0.053)
Washington	0.011 (0.016)

Continent	Estimate
Asia	0.302 (0.155)
North America	0.698 (0.155)